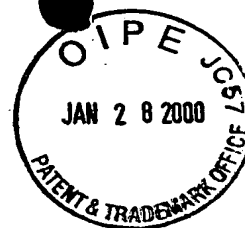


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SEQUENCE LISTING



<110> Hageman, Gregory S.
Kuehn, Markus H.

<120> THERAPEUTICS AND DIAGNOSTICS FOR OCULAR DISEASE BASED
ON A NOVEL HUMAN GENE FAMILY

<130> UIA-027.01

<140> 09/183,972

<141> 1998-10-29

<160> 49

<170> PatentIn Ver. 2.0

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	270					275				280					285	
ggc	tac	aag	gaa	att	cgt	gta	ctt	gaa	ttt	agg	tcc	ccc	aag	gaa	aat	1094
Gly	Tyr	Lys	Glu	Ile	Arg	Val	Leu	Glu	Phe	Arg	Ser	Pro	Lys	Glu	Asn	
			290					295						300		
gac	agt	ggc	gta	gat	gtt	tac	tat	gca	ggt	acc	ttc	aat	ggt	gag	gcc	1142
Asp	Ser	Gly	Val	Asp	Val	Tyr	Tyr	Ala	Val	Thr	Phe	Asn	Gly	Glu	Ala	
			305					310					315			
atc	agc	aat	acc	acc	tgg	gac	ctc	att	agc	ctt	cac	tcc	aac	aag	gtg	1190
Ile	Ser	Asn	Thr	Thr	Trp	Asp	Leu	Ile	Ser	Leu	His	Ser	Asn	Lys	Val	
		320					325					330				
gaa	aac	cat	ggc	ctt	gtg	gaa	ctg	gat	gat	aaa	ccc	act	ggt	ggt	tat	1238
Glu	Asn	His	Gly	Leu	Val	Glu	Leu	Asp	Asp	Lys	Pro	Thr	Val	Val	Tyr	
	335					340					345					
aca	atc	agt	aac	ttc	aga	gat	tat	att	gct	gag	aca	ttg	cag	cag	aat	1286
Thr	Ile	Ser	Asn	Phe	Arg	Asp	Tyr	Ile	Ala	Glu	Thr	Leu	Gln	Gln	Asn	
	350				355					360					365	
ttt	ttg	ctg	ggg	aac	tct	tcc	ttg	aat	cca	gat	cct	gat	tcc	ctg	cag	1334
Phe	Leu	Leu	Gly	Asn	Ser	Ser	Leu	Asn	Pro	Asp	Pro	Asp	Ser	Leu	Gln	
			370					375						380		

ctt atc aat gtg aga gga gtt ttg cgt cac	caa act gaa gat cta gtt	1382
Leu Ile Asn Val Arg Gly Val Leu Arg His	Gln Thr Glu Asp Leu Val	
385	395	
tggt aac acc caa agt tca agt ctt cag gca acg ccg tca tct att ctg	1430	
Trp Asn Thr Gln Ser Ser Ser Leu Gln Ala Thr Pro Ser Ser Ile Leu		
400	405 410	
gat aat acc ttt caa gct gca tgg ccc tca gca gat gaa tcc atc acc	1478	
Asp Asn Thr Phe Gln Ala Ala Trp Pro Ser Ala Asp Glu Ser Ile Thr		
415	420 425	
agc agt att cca cca ctt gat ttc agc tct ggt cct ccc tca gcc act	1526	
Ser Ser Ile Pro Pro Leu Asp Phe Ser Ser Gly Pro Pro Ser Ala Thr		
430	435 440 445	
ggc agg gaa ctc tgg tca gaa agt cct ttg ggt gat tta gtg tct aca	1574	
Gly Arg Glu Leu Trp Ser Glu Ser Pro Leu Gly Asp Leu Val Ser Thr		
450	455 460	
cac aaa tta gcc ttt ccc tcg aag atg ggc ctc agc tct tcc cca gag	1622	
His Lys Leu Ala Phe Pro Ser Lys Met Gly Leu Ser Ser Ser Pro Glu		
465	470 475	
gtt tta gag gtt agc agc ttg act ctt cat tct gtc acc ccg gca gtg	1670	
Val Leu Glu Val Ser Ser Leu Thr Leu His Ser Val Thr Pro Ala Val		
480	485 490	
ctt cag act ggc ttg cct gtg gct tct gag gaa agg act tct gga tct	1718	
Leu Gln Thr Gly Leu Pro Val Ala Ser Glu Glu Arg Thr Ser Gly Ser		
495	500 505	
cac ttg gta gaa gat gga tta gcc aat gtt gaa gag tca gaa gat ttt	1766	
His Leu Val Glu Asp Gly Leu Ala Asn Val Glu Glu Ser Glu Asp Phe		
510	515 520 525	
ctt tct att gat tca ttg cct tca agt tca ttc act caa cct gtg cca	1814	
Leu Ser Ile Asp Ser Leu Pro Ser Ser Ser Phe Thr Gln Pro Val Pro		
530	535 540	
aaa gaa aca ata cca tcc atg gaa gac tct gat gtg tcc tta aca tct	1862	
Lys Glu Thr Ile Pro Ser Met Glu Asp Ser Asp Val Ser Leu Thr Ser		
545	550 555	
tca cca tat ctg acc tct tct ata cct ttt ggc ttg gac tcc ttg acc	1910	
Ser Pro Tyr Leu Thr Ser Ser Ile Pro Phe Gly Leu Asp Ser Leu Thr		
560	565 570	
tcc aaa gtc aaa gac caa tta aaa gtg agc cct ttc ctg cca gat gca	1958	
Ser Lys Val Lys Asp Gln Leu Lys Val Ser Pro Phe Leu Pro Asp Ala		
575	580 585	
tcc atg gaa aaa gag tta ata ttt gac ggt ggt tta ggt tca ggg tct	2006	
Ser Met Glu Lys Glu Leu Ile Phe Asp Gly Gly Leu Gly Ser Gly Ser		
590	595 600 605	

ggg	caa	aag	gta	gat	ctg	att	act	tgg	cca	tgg	agt	gag	act	tca	tca	2054
Gly	Gln	Lys	Val	Asp	Leu	Ile	Thr	Trp	Pro	Trp	Ser	Glu	Thr	Ser	Ser	
				610					615					620		
gag	aag	agc	gcc	gaa	cca	ctg	tcc	aag	ccg	tgg	ctt	gaa	gat	gat	gat	2102
Glu	Lys	Ser	Ala	Glu	Pro	Leu	Ser	Lys	Pro	Trp	Leu	Glu	Asp	Asp	Asp	
			625					630						635		
tca	ctt	ttg	cca	gct	gag	att	gaa	gac	aag	aaa	cta	gtt	tta	gtt	gac	2150
Ser	Leu	Leu	Pro	Ala	Glu	Ile	Glu	Asp	Lys	Lys	Leu	Val	Leu	Val	Asp	
		640					645							650		
aaa	atg	gat	tcc	aca	gac	caa	att	agt	aag	cac	tca	aaa	tat	gaa	cat	2198
Lys	Met	Asp	Ser	Thr	Asp	Gln	Ile	Ser	Lys	His	Ser	Lys	Tyr	Glu	His	
	655					660					665					
gat	gac	aga	tcc	aca	cac	ttt	cca	gag	gaa	gag	cct	ctt	agt	ggg	cct	2246
Asp	Asp	Arg	Ser	Thr	His	Phe	Pro	Glu	Glu	Glu	Pro	Leu	Ser	Gly	Pro	
	670				675					680					685	
gct	gtg	ccc	atc	ttc	gca	gat	act	gca	gct	gaa	tct	gcg	tct	cta	acc	2294
Ala	Val	Pro	Ile	Phe	Ala	Asp	Thr	Ala	Ala	Glu	Ser	Ala	Ser	Leu	Thr	
			690						695						700	
ctc	ccc	aag	cac	ata	tca	gaa	gta	cct	ggg	gtt	gat	gat	tgc	tca	gtt	2342
Leu	Pro	Lys	His	Ile	Ser	Glu	Val	Pro	Gly	Val	Asp	Asp	Cys	Ser	Val	
			705					710						715		
acc	aaa	gca	cct	ctt	ata	ctg	aca	tct	gta	gca	atc	tct	gcc	tct	act	2390
Thr	Lys	Ala	Pro	Leu	Ile	Leu	Thr	Ser	Val	Ala	Ile	Ser	Ala	Ser	Thr	
		720					725						730			
gat	aaa	tca	gat	cag	gca	gat	gcc	atc	cta	agg	gag	gat	atg	gaa	caa	2438
Asp	Lys	Ser	Asp	Gln	Ala	Asp	Ala	Ile	Leu	Arg	Glu	Asp	Met	Glu	Gln	
	735					740					745					
att	act	gag	tca	tcc	aac	tat	gaa	tgg	ttt	gac	agt	gag	gtt	tca	atg	2486
Ile	Thr	Glu	Ser	Ser	Asn	Tyr	Glu	Trp	Phe	Asp	Ser	Glu	Val	Ser	Met	
	750				755					760					765	
gta	aag	cca	gat	atg	caa	act	ttg	tgg	act	ata	ttg	cca	gaa	tca	gag	2534
Val	Lys	Pro	Asp	Met	Gln	Thr	Leu	Trp	Thr	Ile	Leu	Pro	Glu	Ser	Glu	
			770					775						780		
aga	gtt	tgg	aca	aga	act	tct	tcc	cta	gag	aaa	ttg	tcc	aga	gac	ata	2582
Arg	Val	Trp	Thr	Arg	Thr	Ser	Ser	Leu	Glu	Lys	Leu	Ser	Arg	Asp	Ile	
			785					790						795		
ttg	gca	agt	aca	cca	cag	agt	gct	gac	agg	ctc	tgg	tta	tct	gtg	aca	2630
Leu	Ala	Ser	Thr	Pro	Gln	Ser	Ala	Asp	Arg	Leu	Trp	Leu	Ser	Val	Thr	
		800					805							810		
cag	tct	acc	aaa	ttg	cct	cca	acc	aca	atc	tcc	acc	ctg	cta	gag	gat	2678
Gln	Ser	Thr	Lys	Leu	Pro	Pro	Thr	Thr	Ile	Ser	Thr	Leu	Leu	Glu	Asp	
	815					820					825					

gaa gta att atg ggt gta cag gat att tcg tta gaa ctg gac cgg ata	2726
Glu Val Ile Met Gly Val Gln Asp Ile Ser Leu Glu Leu Asp Arg Ile	
830 835 840 845	
ggc aca gat tac tat cag cct gag caa gtc caa gag caa aat ggc aag	2774
Gly Thr Asp Tyr Tyr Gln Pro Glu Gln Val Gln Glu Gln Asn Gly Lys	
850 855 860	
gtt ggt agt tat gtg gaa atg tca aca agt gtt cac tcc aca gag atg	2822
Val Gly Ser Tyr Val Glu Met Ser Thr Ser Val His Ser Thr Glu Met	
865 870 875	
gtt agt gtg gct tgg ccc aca gaa gga gga gat gac ttg agt tat acc	2870
Val Ser Val Ala Trp Pro Thr Glu Gly Gly Asp Asp Leu Ser Tyr Thr	
880 885 890	
cag act tca gga gct ttg gtg gtt ttc ttc agc ctc cga gtg act aac	2918
Gln Thr Ser Gly Ala Leu Val Val Phe Phe Ser Leu Arg Val Thr Asn	
895 900 905	
atg atg ttt tca gaa gat ctg ttt aat aaa aac tcc ttg gag tat aaa	2966
Met Met Phe Ser Glu Asp Leu Phe Asn Lys Asn Ser Leu Glu Tyr Lys	
910 915 920 925	
gcc ctg gag caa aga ttc tta gaa ttg ctg gtt ccc tat ctc cag tca	3014
Ala Leu Glu Gln Arg Phe Leu Glu Leu Leu Val Pro Tyr Leu Gln Ser	
930 935 940	
aat ctc acg ggg ttc cag aac tta gaa atc ctc aac ttc aga aat ggc	3062
Asn Leu Thr Gly Phe Gln Asn Leu Glu Ile Leu Asn Phe Arg Asn Gly	
945 950 955	
agc att gtg gtg aac agt cga atg aag ttt gcc aat tct gtc cct cct	3110
Ser Ile Val Val Asn Ser Arg Met Lys Phe Ala Asn Ser Val Pro Pro	
960 965 970	
aac gtc aac aat gcg gtg tac atg att ctg gaa gac ttt tgt acc act	3158
Asn Val Asn Asn Ala Val Tyr Met Ile Leu Glu Asp Phe Cys Thr Thr	
975 980 985	
gcc tac aat acc atg aac ttg gct att gat aaa tac tct ctt gat gtg	3206
Ala Tyr Asn Thr Met Asn Leu Ala Ile Asp Lys Tyr Ser Leu Asp Val	
990 995 1000 1005	
gaa tca ggt gat gaa gcc aac cct tgc aag ttt cag gcc tgt aat gaa	3254
Glu Ser Gly Asp Glu Ala Asn Pro Cys Lys Phe Gln Ala Cys Asn Glu	
1010 1015 1020	
ttt tca gag tgt ctg gtc aac ccc tgg agt gga gaa gca aag tgc aga	3302
Phe Ser Glu Cys Leu Val Asn Pro Trp Ser Gly Glu Ala Lys Cys Arg	
1025 1030 1035	
tgc ttc cct gga tac ctg agt gtg gaa gaa cgg ccc tgt cag agt ctc	3350
Cys Phe Pro Gly Tyr Leu Ser Val Glu Glu Arg Pro Cys Gln Ser Leu	
1040 1045 1050	

tgt gac cta cag cct gac ttc tgc ttg aat gat gga aag tgt gac att 3398
 Cys Asp Leu Gln Pro Asp Phe Cys Leu Asn Asp Gly Lys Cys Asp Ile
 1055 1060 1065

atg cct ggg cac ggg gcc att tgt agg tgc cgg gtg ggt gag aac tgg 3446
 Met Pro Gly His Gly Ala Ile Cys Arg Cys Arg Val Gly Glu Asn Trp
 1070 1075 1080 1085

tgg tac cga ggc aag cac tgt gag gaa ttt gtg tct gag ccc gtg atc 3494
 Trp Tyr Arg Gly Lys His Cys Glu Glu Phe Val Ser Glu Pro Val Ile
 1090 1095 1100

ata ggc atc act att gcc tcc gtg gtt gga ctt ctt gtc atc ttt tct 3542
 Ile Gly Ile Thr Ile Ala Ser Val Val Gly Leu Leu Val Ile Phe Ser
 1105 1110 1115

gct atc atc tac ttc ttc atc agg act ctt caa gca cac cat gac agg 3590
 Ala Ile Ile Tyr Phe Phe Ile Arg Thr Leu Gln Ala His His Asp Arg
 1120 1125 1130

agt gaa aga gag agt ccc ttc agt ggc tcc agc agg cag cct gac agc 3638
 Ser Glu Arg Glu Ser Pro Phe Ser Gly Ser Ser Arg Gln Pro Asp Ser
 1135 1140 1145

ctc tca tct att gag aat gct gtg aag tac aac ccc gtg tat gaa agt 3686
 Leu Ser Ser Ile Glu Asn Ala Val Lys Tyr Asn Pro Val Tyr Glu Ser
 1150 1155 1160 1165

cac agg gct gga tgt gag aag tat gag gga ccc tat cct cag cat ccc 3734
 His Arg Ala Gly Cys Glu Lys Tyr Glu Gly Pro Tyr Pro Gln His Pro
 1170 1175 1180

ttc tac agc tct gct agc gga gac gtg att ggt ggg ctg agc aga gaa 3782
 Phe Tyr Ser Ser Ala Ser Gly Asp Val Ile Gly Gly Leu Ser Arg Glu
 1185 1190 1195

gaa atc aga cag atg tat gag agc agt gag ctt tcc aga gag gaa att 3830
 Glu Ile Arg Gln Met Tyr Glu Ser Ser Glu Leu Ser Arg Glu Glu Ile
 1200 1205 1210

caa gag aga atg aga gtt ttg gaa ctg tat gcc aat gat cct gag ttt 3878
 Gln Glu Arg Met Arg Val Leu Glu Leu Tyr Ala Asn Asp Pro Glu Phe
 1215 1220 1225

gca gct ttt gtg aga gag caa caa gtg gaa gag gtt taaccaaacc 3924
 Ala Ala Phe Val Arg Glu Gln Gln Val Glu Glu Val
 1230 1235 1240

tcctgttctg aaactgatta gaagcctgga gaagatggag attacttggt acttatgtca 3984

tataattaac ctggatttta aacactgttg gaagaagagn tttctatgaa aaaattaaat 4044

atagggcaca ctgttttttt ttcagcttaa gntttcagaa tgtagtnaga gatgtwmcac 4104

ttttattttct ataaagactg aatgctgtgt ttaaataatt gaaaactacg ttaaaaaaaaa 4164

a 4165

<210> 6
<211> 1241
<212> PRT
<213> Homo sapiens

<400> 6
Met Ile Met Phe Pro Leu Phe Gly Lys Ile Ser Leu Gly Ile Leu Ile
1 5 10 15
Phe Val Leu Ile Glu Gly Asp Phe Pro Ser Leu Thr Ala Gln Thr Tyr
20 25 30
Leu Ser Ile Glu Glu Ile Gln Glu Pro Lys Ser Ala Val Ser Phe Leu
35 40 45
Leu Pro Glu Glu Ser Thr Asp Leu Ser Leu Ala Thr Lys Lys Lys Gln
50 55 60
Pro Leu Asp Arg Arg Glu Thr Glu Arg Gln Trp Leu Ile Arg Arg Arg
65 70 75 80
Arg Ser Ile Leu Phe Pro Asn Gly Val Lys Ile Cys Pro Asp Glu Ser
85 90 95
Val Ala Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys Val Arg Val
100 105 110
Cys Gln Glu Ala Val Trp Glu Ala Phe Arg Thr Phe Trp Asp Arg Leu
115 120 125
Pro Gly Arg Glu Glu Tyr His Tyr Trp Met Asn Leu Cys Glu Asp Gly
130 135 140
Val Thr Ser Ile Phe Glu Met Gly Thr Asn Phe Ser Glu Ser Val Glu
145 150 155 160
His Arg Ser Leu Ile Met Lys Lys Leu Thr Tyr Ala Lys Glu Thr Val
165 170 175
Ser Ser Ser Glu Leu Ser Ser Pro Val Pro Val Gly Asp Thr Ser Thr
180 185 190
Leu Gly Asp Thr Thr Leu Ser Val Pro His Pro Glu Val Asp Ala Tyr
195 200 205
Glu Gly Ala Ser Glu Ser Ser Leu Glu Arg Pro Glu Glu Ser Ile Ser
210 215 220
Asn Glu Ile Glu Asn Val Ile Glu Glu Ala Thr Lys Pro Ala Gly Glu
225 230 235 240
Gln Ile Ala Glu Phe Ser Ile His Leu Leu Gly Lys Gln Tyr Arg Glu
245 250 255
Glu Leu Gln Asp Ser Ser Ser Phe His His Gln His Leu Glu Glu Glu
260 265 270

Phe Ile Ser Glu Val Glu Asn Ala Phe Thr Gly Leu Pro Gly Tyr Lys
 275 280 285
 Glu Ile Arg Val Leu Glu Phe Arg Ser Pro Lys Glu Asn Asp Ser Gly
 290 295 300
 Val Asp Val Tyr Tyr Ala Val Thr Phe Asn Gly Glu Ala Ile Ser Asn
 305 310 315 320
 Thr Thr Trp Asp Leu Ile Ser Leu His Ser Asn Lys Val Glu Asn His
 325 330 335
 Gly Leu Val Glu Leu Asp Asp Lys Pro Thr Val Val Tyr Thr Ile Ser
 340 345 350
 Asn Phe Arg Asp Tyr Ile Ala Glu Thr Leu Gln Gln Asn Phe Leu Leu
 355 360 365
 Gly Asn Ser Ser Leu Asn Pro Asp Pro Asp Ser Leu Gln Leu Ile Asn
 370 375 380
 Val Arg Gly Val Leu Arg His Gln Thr Glu Asp Leu Val Trp Asn Thr
 385 390 395 400
 Gln Ser Ser Ser Leu Gln Ala Thr Pro Ser Ser Ile Leu Asp Asn Thr
 405 410 415
 Phe Gln Ala Ala Trp Pro Ser Ala Asp Glu Ser Ile Thr Ser Ser Ile
 420 425 430
 Pro Pro Leu Asp Phe Ser Ser Gly Pro Pro Ser Ala Thr Gly Arg Glu
 435 440 445
 Leu Trp Ser Glu Ser Pro Leu Gly Asp Leu Val Ser Thr His Lys Leu
 450 455 460
 Ala Phe Pro Ser Lys Met Gly Leu Ser Ser Ser Pro Glu Val Leu Glu
 465 470 475 480
 Val Ser Ser Leu Thr Leu His Ser Val Thr Pro Ala Val Leu Gln Thr
 485 490 495
 Gly Leu Pro Val Ala Ser Glu Glu Arg Thr Ser Gly Ser His Leu Val
 500 505 510
 Glu Asp Gly Leu Ala Asn Val Glu Glu Ser Glu Asp Phe Leu Ser Ile
 515 520 525
 Asp Ser Leu Pro Ser Ser Ser Phe Thr Gln Pro Val Pro Lys Glu Thr
 530 535 540
 Ile Pro Ser Met Glu Asp Ser Asp Val Ser Leu Thr Ser Ser Pro Tyr
 545 550 555 560
 Leu Thr Ser Ser Ile Pro Phe Gly Leu Asp Ser Leu Thr Ser Lys Val
 565 570 575

Lys	Asp	Gln	Leu	Lys	Val	Ser	Pro	Phe	Leu	Pro	Asp	Ala	Ser	Met	Glu	580	585	590
Lys	Glu	Leu	Ile	Phe	Asp	Gly	Gly	Leu	Gly	Ser	Gly	Ser	Gly	Gln	Lys	595	600	605
Val	Asp	Leu	Ile	Thr	Trp	Pro	Trp	Ser	Glu	Thr	Ser	Ser	Glu	Lys	Ser	610	615	620
Ala	Glu	Pro	Leu	Ser	Lys	Pro	Trp	Leu	Glu	Asp	Asp	Asp	Ser	Leu	Leu	625	630	635
Pro	Ala	Glu	Ile	Glu	Asp	Lys	Lys	Leu	Val	Leu	Val	Asp	Lys	Met	Asp	645	650	655
Ser	Thr	Asp	Gln	Ile	Ser	Lys	His	Ser	Lys	Tyr	Glu	His	Asp	Asp	Arg	660	665	670
Ser	Thr	His	Phe	Pro	Glu	Glu	Glu	Pro	Leu	Ser	Gly	Pro	Ala	Val	Pro	675	680	685
Ile	Phe	Ala	Asp	Thr	Ala	Ala	Glu	Ser	Ala	Ser	Leu	Thr	Leu	Pro	Lys	690	695	700
His	Ile	Ser	Glu	Val	Pro	Gly	Val	Asp	Asp	Cys	Ser	Val	Thr	Lys	Ala	705	710	715
Pro	Leu	Ile	Leu	Thr	Ser	Val	Ala	Ile	Ser	Ala	Ser	Thr	Asp	Lys	Ser	725	730	735
Asp	Gln	Ala	Asp	Ala	Ile	Leu	Arg	Glu	Asp	Met	Glu	Gln	Ile	Thr	Glu	740	745	750
Ser	Ser	Asn	Tyr	Glu	Trp	Phe	Asp	Ser	Glu	Val	Ser	Met	Val	Lys	Pro	755	760	765
Asp	Met	Gln	Thr	Leu	Trp	Thr	Ile	Leu	Pro	Glu	Ser	Glu	Arg	Val	Trp	770	775	780
Thr	Arg	Thr	Ser	Ser	Leu	Glu	Lys	Leu	Ser	Arg	Asp	Ile	Leu	Ala	Ser	785	790	795
Thr	Pro	Gln	Ser	Ala	Asp	Arg	Leu	Trp	Leu	Ser	Val	Thr	Gln	Ser	Thr	805	810	815
Lys	Leu	Pro	Pro	Thr	Thr	Ile	Ser	Thr	Leu	Leu	Glu	Asp	Glu	Val	Ile	820	825	830
Met	Gly	Val	Gln	Asp	Ile	Ser	Leu	Glu	Leu	Asp	Arg	Ile	Gly	Thr	Asp	835	840	845
Tyr	Tyr	Gln	Pro	Glu	Gln	Val	Gln	Glu	Gln	Asn	Gly	Lys	Val	Gly	Ser	850	855	860
Tyr	Val	Glu	Met	Ser	Thr	Ser	Val	His	Ser	Thr	Glu	Met	Val	Ser	Val	865	870	875
																880		

Ala Trp Pro Thr	Glu Gly Gly Asp Asp	Leu Ser Tyr Thr Gln Thr Ser
885		890 895
Gly Ala Leu Val Val Phe Phe Ser	Leu Arg Val Thr Asn Met Met Phe	
900	905	910
Ser Glu Asp Leu Phe Asn Lys Asn	Ser Leu Glu Tyr Lys Ala Leu Glu	
915	920	925
Gln Arg Phe Leu Glu Leu Leu Val	Pro Tyr Leu Gln Ser Asn Leu Thr	
930	935	940
Gly Phe Gln Asn Leu Glu Ile Leu	Asn Phe Arg Asn Gly Ser Ile Val	
945	950	955 960
Val Asn Ser Arg Met Lys Phe Ala	Asn Ser Val Pro Pro Asn Val Asn	
965	970	975
Asn Ala Val Tyr Met Ile Leu Glu	Asp Phe Cys Thr Thr Ala Tyr Asn	
980	985	990
Thr Met Asn Leu Ala Ile Asp Lys	Tyr Ser Leu Asp Val Glu Ser Gly	
995	1000	1005
Asp Glu Ala Asn Pro Cys Lys Phe	Gln Ala Cys Asn Glu Phe Ser Glu	
1010	1015	1020
Cys Leu Val Asn Pro Trp Ser Gly	Glu Ala Lys Cys Arg Cys Phe Pro	
025	1030	1035 1040
Gly Tyr Leu Ser Val Glu Glu Arg	Pro Cys Gln Ser Leu Cys Asp Leu	
1045	1050	1055
Gln Pro Asp Phe Cys Leu Asn Asp	Gly Lys Cys Asp Ile Met Pro Gly	
1060	1065	1070
His Gly Ala Ile Cys Arg Cys Arg	Val Gly Glu Asn Trp Trp Tyr Arg	
1075	1080	1085
Gly Lys His Cys Glu Glu Phe Val	Ser Glu Pro Val Ile Ile Gly Ile	
1090	1095	1100
Thr Ile Ala Ser Val Val Gly Leu Leu Val Ile Phe Ser Ala Ile Ile		
105	1110	1115 1120
Tyr Phe Phe Ile Arg Thr Leu Gln Ala His His Asp Arg Ser Glu Arg		
1125	1130	1135
Glu Ser Pro Phe Ser Gly Ser Ser Arg Gln Pro Asp Ser Leu Ser Ser		
1140	1145	1150
Ile Glu Asn Ala Val Lys Tyr Asn Pro Val Tyr Glu Ser His Arg Ala		
1155	1160	1165
Gly Cys Glu Lys Tyr Glu Gly Pro Tyr Pro Gln His Pro Phe Tyr Ser		
1170	1175	1180

Ser Ala Ser Gly Asp Val Ile Gly Gly Leu Ser Arg Glu Glu Ile Arg
 185 1190 1195 1200

Gln Met Tyr Glu Ser Ser Glu Leu Ser Arg Glu Glu Ile Gln Glu Arg
 1205 1210 1215

Met Arg Val Leu Glu Leu Tyr Ala Asn Asp Pro Glu Phe Ala Ala Phe
 1220 1225 1230

Val Arg Glu Gln Gln Val Glu Glu Val
 1235 1240

<210> 7
 <211> 20
 <212> PRT
 <213> rattus

<400> 7
 Ser Ile Leu Phe Pro Asn Gly Val Arg Ile Cys Pro Ser Asp Thr Val
 1 5 10 15

Ala Glu Ala Val
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<210> 8
 <211> 20
 <212> PRT
 <213> porcine

<220>
 <221> UNSURE
 <222> (1)..(20)
 <223> applicants are unsure of residues designated as
 "Xaa" at positions 1 & 11

<400> 8
 Xaa Val Phe Phe Pro Thr Gly Val Lys Val Xaa Pro Gln Glu Ser Met
 1 5 10 15

Lys Gln Ile Leu
 20

<210> 9
 <211> 10
 <212> PRT
 <213> porcine

<220>
 <221> UNSURE
 <222> (1)..(10)
 <223> applicants are unsure of residues designated as
 "Xaa" at position 1

<400> 9
 Xaa Val Leu Phe Pro Asn Gly Val Lys Ile
 1 5 10

<210> 10
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <221> modified_base
 <222> (25)
 <223> i

<400> 10
 tattaggaat tccatyttyt tyccnaaygg

30

<210> 11
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer
 <220>
 <221> modified_base
 <222> (1)..(26)
 <223> "n" at positions 3, 6, 9 & 24 represent "inosine"

<400> 11
 ttncncngcna gytcytrta rtangg

26

<210> 12
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 12
 ggatttttct ccaagttcaa gg

22

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 13
acgggggtta aagtctgtcc

20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
cgaacaaaaa gatccgcatt

20

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<400> 15
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21

<210> 16
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<220>
<223> Description of Artificial Sequence: primer

<400> 16
atcaggactg ggtcagcatc

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<210> 17
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<220>
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<400> 17
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<223> Description of Artificial Sequence: primer

<400> 18

gagcctgggtg aaaccattgt

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<210> 19

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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gtggagctca gcgtctctct

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<210> 20

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 20

tgtgttggag gagcagagg

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<210> 21

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<223> Description of Artificial Sequence: primer

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<210> 22

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 22

gaaacttcca ggattcaaaa aa

22

<210> 23

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

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<400> 23

aggaggacaa gcaaccagaa

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<210> 24

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 24

tccaacaaaa ttgaaagtga gg

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<210> 25

<211> 20

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<400> 25

aatcagagct gccacatct

20

<210> 26

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 26

agcctttggt cctgacacc

19

<210> 27

<211> 21

<212> DNA

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<400> 27

ccacctttct ttatggcatc a

21

<210> 28

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<220>
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<400> 28
agtcaggtg gcgaagatat

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<210> 29
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<400> 29
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<210> 30
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<220>
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<400> 30
ccacctgcat cttcagatga ca

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<210> 31
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<220>
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<400> 31
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<210> 32
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<212> DNA
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<220>
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<400> 32
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22

<210> 33
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<220>
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<400> 33
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21

<210> 34
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<400> 34
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<210> 35
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<220>
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<400> 35
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<210> 36
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<212> DNA
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<220>
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<400> 36
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<210> 37
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<400> 37

gactgaggaa gcggagtgtc

20

<210> 38
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<220>
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<400> 38
acgaacggac tgaggaag

18

<210> 39
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 39
ttctgaatta ctgaccgtag aa

22

<210> 40
<211> 22
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<220>
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<400> 40
ttccaaaatc aacaaaataa ca

22

<210> 41
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<220>
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<400> 41
ggtcacataa atccagacat a

21

<210> 42
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<220>
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<400> 42
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27

<210> 43
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 <212> DNA
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<220>
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<400> 43
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20

<210> 44
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<220>
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.<400> 44
 taaaacccca aatgcaatca

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<210> 45
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 45
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21

<210> 46
 <211> 15
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(15)
 <223> applicants are unsure of residues designated as
 "Xaa" at positions 1 & 11

<400> 46
 Xaa Ala Leu Phe Pro Asn Gly Val Leu Ile Xaa Pro Xaa Glu Val
 1 5 10 15

<210> 47

<211> 19
 <212> PRT
 <213> Callimico sp.

<220>
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 <222> (1)..(19)
 <223> applicants are unsure of residues designated as
 "Xaa" at positions 1, 11 & 16

<400> 47
 Xaa Ile Leu Phe Pro Asn Gly Val Leu Ile Xaa Pro Asp Glu Val Xaa
 1 5 10 15

Lys Glu Ile

<210> 48
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 48
 Ser Ala Phe Phe Pro Thr Gly Val Lys Val Cys Pro Gln Glu Ser Met
 1 5 10 15

Lys Gln Ile Leu
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<210> 49
 <211> 18
 <212> PRT
 <213> Callimico sp.

<220>
 <221> UNSURE
 <222> (1)..(18)
 <223> applicants are unsure of residues designated as
 "Xaa" at positions 1 & 11

<400> 49
 Xaa Ile Phe Phe Pro Thr Gly Val Lys Val Xaa Pro Gln Glu Ser Met
 1 5 10 15

Lys Gln